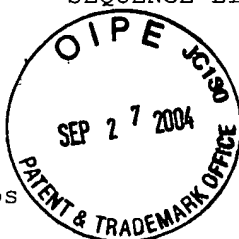


## SEQUENCE LISTING

<110> Pompejus, Markus  
 Seulberger, Harald  
 Hoeffken, Hans Wolfgang  
 Doval, Jose Luis Revuelta  
 Jimenez, Alberto  
 Garcia, Maria Angeles Santos



<120> Phosphoriboxyl-Pyrophosphate Synthetase Polypeptide

<130> PF48687-2/DP

<140> US 10/076,157

<141> 2002-02-15

<150> Germany, 19757755.5

<151> 1997-12-23

<160> 21

<170> WordPerfect 8

<210> 1

<211> 1911

<212> DNA

<213> Ashbya gossypii

<400> 1

GGTAGTCGCT CATCGACAGA CACAATCGCG TGTTCTCTCT GAATCGTCCA TTGGGTGTCA	60
GCATCCTGAT CGCGGGCGGA TGGAATGGGT AATCATTAGG AAACACCAAT GTCCCATGGT	120
ATTGTCCGTC CTCGTATGGT GTCTCAGGAG GACCCGTGAT CACGTAGTGC CACACCAGGA	180
TATTGTCTTC CTTTGGTGCT GCCACGATGT AGGGCGGGGG GTTCTCGGTC ATCATTTTGT	240
ACTCCTTTGA GAGCCGCTTG TACGCCTGTC TTGATGCCAT CTTGCCTACT ATTAGTTTCT	300
CACCACTTCC CGCCAAACAA TCTGCACTTT ACGAGCGCTA TCTATCCCTC GGGTCGCTCT	360
AGTTGATTAT TGGCGAAACT GATAGTTCAG GTACTTCCAT GATGCGGTCA TATCCACGTA	420
TGTGATCACG TGATCATCAG CCATGCTGCC AGCTCACGGG CCTGCCTACA CTATTGGAGG	480
CTCTGTGAGT CATGATTTAT TGCATATCAA GCCCAGATAG TCGTTGGGGA TACTACCGTT	540
GCCGCGATGA GCTCCGATAT TAAGTTGTAG CCAAAAATTT TAACGGATGA CTTCTTAACA	600
GTTATTGACG CCGCAATCCT ACGCC ATG TCG TCC AAT AGC ATA AAG CTG CTA	652
Met Ser Ser Asn Ser Ile Lys Leu Leu	
1 5	
GCA GGT AAC TCG CAC CCG GAC CTA GCT GAG AAG GTC TCC GTT CGC CTA	700
Ala Gly Asn Ser His Pro Asp Leu Ala Glu Lys Val Ser Val Arg Leu	
10 15 20 25	
GGT GTA CCA CTT TCG AAG ATT GGA GTG TAT CAC TAC TCT AAC AAA GAG	748
Gly Val Pro Leu Ser Lys Ile Gly Val Tyr His Tyr Ser Asn Lys Glu	

30										35					40					
ACG	TCA	GTT	ACT	ATC	GGC	GAA	AGT	ATC	CGT	GAT	GAA	GAT	GTC	TAC	ATC	796				
Thr	Ser	Val	Thr	Ile	Gly	Glu	Ser	Ile	Arg	Asp	Glu	Asp	Val	Tyr	Ile					
			45					50					55							
ATC	CAG	ACA	GGA	ACG	GGG	GAG	CAG	GAA	ATC	AAC	GAC	TTC	CTC	ATG	GAA	844				
Ile	Gln	Thr	Gly	Thr	Gly	Glu	Gln	Glu	Ile	Asn	Asp	Phe	Leu	Met	Glu					
		60					65					70								
CTG	CTC	ATC	ATG	ATC	CAT	GCC	TGC	CGG	TCA	GCC	TCT	GCG	CGG	AAG	ATC	892				
Leu	Leu	Ile	Met	Ile	His	Ala	Cys	Arg	Ser	Ala	Ser	Ala	Arg	Lys	Ile					
	75					80					85									
ACA	GCG	GTT	ATA	CCA	AAC	TTC	CCT	TAC	GCA	AGA	CAA	GAC	AAA	AAG	GAC	940				
Thr	Ala	Val	Ile	Pro	Asn	Phe	Pro	Tyr	Ala	Arg	Gln	Asp	Lys	Lys	Asp					
	90				95				100						105					
AAG	TCG	CGA	GCA	CCG	ATA	ACT	GCC	AAG	CTG	GTG	GCC	AAG	ATG	CTA	GAG	988				
Lys	Ser	Arg	Ala	Pro	Ile	Thr	Ala	Lys	Leu	Val	Ala	Lys	Met	Leu	Glu					
				110					115					120						
ACC	GCG	GGG	TGC	AAC	CAC	GTT	ATC	ACG	ATG	GAT	TTG	CAC	GCG	TCT	CAA	1036				
Thr	Ala	Gly	Cys	Asn	His	Val	Ile	Thr	Met	Asp	Leu	His	Ala	Ser	Gln					
			125					130					135							
ATT	CAG	GGT	TTC	TTC	CAC	ATT	CCA	GTG	GAC	AAC	CTA	TAT	GCA	GAG	CCG	1084				
Ile	Gln	Gly	Phe	Phe	His	Ile	Pro	Val	Asp	Asn	Leu	Tyr	Ala	Glu	Pro					
		140					145					150								
AAC	ATC	CTG	CAC	TAC	ATC	CAA	CAT	AAT	GTG	GAC	TTC	CAG	AAT	AGT	ATG	1132				
Asn	Ile	Leu	His	Tyr	Ile	Gln	His	Asn	Val	Asp	Phe	Gln	Asn	Ser	Met					
	155					160					165									
TTG	GTC	GCG	CCA	GAC	GCG	GGG	TCG	GCG	AAG	CGC	ACG	TCG	ACG	CTT	TCG	1180				
Leu	Val	Ala	Pro	Asp	Ala	Gly	Ser	Ala	Lys	Arg	Thr	Ser	Thr	Leu	Ser					
	170				175					180					185					
GAC	AAG	CTG	AAT	CTC	AAC	TTC	GCG	TTG	ATC	CAC	AAA	GAA	CGG	CAG	AAG	1228				
Asp	Lys	Leu	Asn	Leu	Asn	Phe	Ala	Leu	Ile	His	Lys	Glu	Arg	Gln	Lys					
				190					195					200						
GCG	AAC	GAG	GTC	TCG	CGG	ATG	GTG	TTG	GTG	GGT	GAT	GTC	GCC	GAC	AAG	1276				
Ala	Asn	Glu	Val	Ser	Arg	Met	Val	Leu	Val	Gly	Asp	Val	Ala	Asp	Lys					
			205					210					215							
TCC	TGT	ATT	ATT	GTA	GAC	GAC	ATG	GCG	GAC	ACG	TGC	GGA	ACG	CTA	GTG	1324				
Ser	Cys	Ile	Ile	Val	Asp	Asp	Met	Ala	Asp	Thr	Cys	Gly	Thr	Leu	Val					
		220					225					230								
AAG	GCC	ACT	GAC	ACG	CTG	ATC	GAA	AAT	TGT	GCG	AAA	GAA	GTG	ATT	GCC	1372				
Lys	Ala	Thr	Asp	Thr	Leu	Ile	Glu	Asn	Cys	Ala	Lys	Glu	Val	Ile	Ala					
	235					240					245									
ATT	GTG	ACA	CAC	GGT	ATA	TTT	TCT	GGC	GGC	GCC	CGC	GAG	AAG	TTG	CGC	1420				
Ile	Val	Thr	His	Gly	Ile	Phe	Ser	Gly	Gly	Ala	Arg	Glu	Lys	Leu	Arg					
	250				255					260					265					
AAC	AGC	AAG	CTG	GCA	CGG	ATC	GTA	AGC	ACA	AAT	ACG	GTG	CCA	GTG	GAC	1468				
Asn	Ser	Lys	Leu	Ala	Arg	Ile	Val	Ser	Thr	Asn	Thr	Val	Pro	Val	Asp					

270	275	280	
CTC AAT CTA GAT ATC TAC CAC CAA ATT GAC ATT AGT GCC ATT TTG GCC			1516
Leu Asn Leu Asp Ile Tyr His Gln Ile Asp Ile Ser Ala Ile Leu Ala			
285	290	295	
GAG GCA ATT AGA AGG CTT CAC AAC GGG GAA AGT GTG TCG TAC CTG TTC			1564
Glu Ala Ile Arg Arg Leu His Asn Gly Glu Ser Val Ser Tyr Leu Phe			
300	305	310	
AAT AAC GCT GTC ATG TAGTGCTGTC AGTGGCAGAT GCATGATCGC TGGCCTAATT			1619
Asn Asn Ala Val Met			
315			
ATCTGTGTAA GTTGATACAA TGCAGTAAAT ACAGTACATA AAACTGAATG TTTTTCACCTT			1679
AGGGGTGCTT TGTGTCTCTG ATAGCGTGTG TGCGAATTTG GAGGTGAAAG TTGAACATCA			1739
CGTAATGAAT ACAAACAAGA TTGCACATTA GGAAAAGCGA TAAATTATTT ATTATTTGCA			1799
ACTGGCCTTT GAGCGTTTAA GCCTGAACAT TTTTGCCCTT TTGTTTGACC GTACCGTTAT			1859
CACTCGTCCT TATATATGGC TATCCTTCTC TTCCGGAAC TCTTCGAGCG TA			1911
<210> 2			
<211> 318			
<212> PRT			
<213> Ashbya gossypii			
<400> 2			
Met Ser Ser Asn Ser Ile Lys Leu Leu Ala Gly Asn Ser His Pro Asp			
1	5	10	15
Leu Ala Glu Lys Val Ser Val Arg Leu Gly Val Pro Leu Ser Lys Ile			
20	25	30	
Gly Val Tyr His Tyr Ser Asn Lys Glu Thr Ser Val Thr Ile Gly Glu			
35	40	45	
Ser Ile Arg Asp Glu Asp Val Tyr Ile Ile Gln Thr Gly Thr Gly Glu			
50	55	60	
Gln Glu Ile Asn Asp Phe Leu Met Glu Leu Leu Ile Met Ile His Ala			
65	70	75	80
Cys Arg Ser Ala Ser Ala Arg Lys Ile Thr Ala Val Ile Pro Asn Phe			
85	90	95	
Pro Tyr Ala Arg Gln Asp Lys Lys Asp Lys Ser Arg Ala Pro Ile Thr			
100	105	110	
Ala Lys Leu Val Ala Lys Met Leu Glu Thr Ala Gly Cys Asn His Val			
115	120	125	
Ile Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe His Ile			
130	135	140	
Pro Val Asp Asn Leu Tyr Ala Glu Pro Asn Ile Leu His Tyr Ile Gln			

145		150		155		160
His Asn Val Asp	Phe Gln Asn Ser Met	Leu Val Ala Pro Asp	Ala Gly			
	165	170	175			
Ser Ala Lys Arg	Thr Ser Thr Leu Ser	Asp Lys Leu Asn	Leu Asn Phe			
	180	185	190			
Ala Leu Ile His	Lys Glu Arg Gln Lys	Ala Asn Glu Val	Ser Arg Met			
	195	200	205			
Val Leu Val Gly	Asp Val Ala Asp	Lys Ser Cys Ile	Ile Val Asp Asp			
	210	215	220			
Met Ala Asp Thr	Cys Gly Thr Leu Val	Lys Ala Thr Asp	Thr Leu Ile			
	225	230	235			240
Glu Asn Cys Ala	Lys Glu Val Ile Ala	Ile Val Thr His	Gly Ile Phe			
	245	250	255			
Ser Gly Gly Ala	Arg Glu Lys Leu Arg	Asn Ser Lys Leu	Ala Arg Ile			
	260	265	270			
Val Ser Thr Asn	Thr Val Pro Val	Asp Leu Asn Leu	Asp Ile Tyr His			
	275	280	285			
Gln Ile Asp Ile	Ser Ala Ile Leu Ala	Glu Ala Ile Arg	Arg Leu His			
	290	295	300			
Asn Gly Glu Ser	Val Ser Tyr Leu Phe	Asn Asn Ala Val	Met			
	305	310	315			

<210> 3  
 <211> 5369  
 <212> DNA  
 <213> Ashbya gossypii  
 <400> 3

AAGCTTGACC TTGGCTGGCA CTTGAGTCGG CAGACAGGTG GACTAACCCG AGCA	ATG	57
	Met	
	1	
GAT CGT GGT TGT AAA GGT ATC TCT TAT GTG CTC AGT GCA ATG GTT TTT		105
Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val Phe		
	5 10 15	
CAC ATA ATA CCG ATT ACA TTT GAA ATA TCG ATG GTA TGT GGC ATA TTG		153
His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile Leu		
	20 25 30	
ACA TAC CAG TTT GGT GCT TCC TTC GCT GCT ATA ACA TTC TCG ACT ATG		201
Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr Met		
	35 40 45	
CTT CTT TAC TCC ATC TTT ACT TTC AGA ACG ACG GCG TGG CGC ACA CGG		249
Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr Arg		
	50 55 60 65	

TTT AGG CGT GAT GCG AAC AAG GCT GAC AAT AAG GCC GCT AGT GTG GCA	297
Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val Ala	
70 75 80	
TTG GAT TCC CTA ATA AAT TTT GAA GCT GTA AAG TAT TTC AAT AAC GAG	345
Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn Glu	
85 90 95	
AAG TAC CTT GCG GAC AAG TAT CAC ACA TCC TTG ATG AAG TAC CGG GAT	393
Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg Asp	
100 105 110	
TCC CAG ATA AAG GTC TCG CAA TCG CTG GCG TTT TTG AAC ACC GGC CAG	441
Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly Gln	
115 120 125	
AAC CTA ATT TTT ACC ACT GCA CTG ACT GCA ATG ATG TAT ATG GCC TGT	489
Asn Leu Ile Phe Thr Ala Leu Thr Ala Met Met Tyr Met Ala Cys	
130 135 140 145	
AAT GGT GTT ATG CAG GGC TCT CTT ACA GTG GGG GAT CTT GTG TTA ATT	537
Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu Ile	
150 155 160	
AAT CAA CTG GTA TTC CAG CTC TCC GTG CCA CTA AAC TTC CTT GGT AGC	585
Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly Ser	
165 170 175	
GTC TAC CGT GAT CTC AAG CAG TCT CTG ATA GAT ATG GAA TCT TTA TTT	633
Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu Phe	
180 185 190	
AAA CTG CAA AAA AAT CAG GTC ACA ATT AAG AAC TCC CCA AAT GCC CAG	681
Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala Gln	
195 200 205	
AAC CTA CCA ATA CAC AAA CCG TTG GAT ATT CGC TTT GAA AAT GTT ACG	729
Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val Thr	
210 215 220 225	
TTT GGC TAT GAC CCG GAG CGG CGT ATA TTG AAC AAT GTT TCG TTT ACC	777
Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe Thr	
230 235 240	
ATC CCA GCT GGA ATG AAG ACT GCC ATA GTA GGC CCA TCG GGC TCG GGG	825
Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser Gly	
245 250 255	
AAG TCC ACC ATT TTG AAG CTC GTA TTT AGA TTC TAT GAG CCC GAG CAA	873
Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu Gln	
260 265 270	
GGT CGT ATC CTA GTT GGC GGC ACA GAT ATC CGC GAT TTA GAC TTG CTT	921
Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu Leu	
275 280 285	
TCT TTA CGG AAG GCT ATC GGT GTC GTG CCC CAA GAT ACT CCT CTC TTC	969
Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu Phe	
290 295 300 305	

AAT GAC ACA ATC TGG GAG AAT GTT AAA TTC GGC AAT ATC AGT TCC TCT	1017
Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser Ser	
310 315 320	
GAC GAT GAG ATT CTC AGG GCC ATA GAA AAA GCT CAA CTC ACG AAG CTA	1065
Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys Leu	
325 330 335	
CTC CAG AAC CTA CCA AAG GGC GCT TCC ACC GTT GTA GGG GAG CGC GGT	1113
Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg Gly	
340 345 350	
TTG ATG ATC AGC GGA GGT GAG AAA CAA AGG CTT GCT ATT GCT CGT GTG	1161
Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg Val	
355 360 365	
CTT TTG AAG GAC GCT CCG CTG ATG TTT TTC GAC GAG GCT ACA AGT GCT	1209
Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser Ala	
370 375 380 385	
CTG GAT ACA CAC ACA GAG CAG GCA CTC TTG CAC ACC ATT CAG CAG AAC	1257
Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln Asn	
390 395 400	
TTT TCT TCC AAT TCA AAG ACG AGC GTT TAC GTT GCC CAT AGA CTG CGC	1305
Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu Arg	
405 410 415	
ACA ATC GCT GAT GCA GAT AAG ATC ATT GTT CTT GAA CAA GGT TCT GTC	1353
Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser Val	
420 425 430	
CGC GAA GAG GGC ACA CAC AGC TCG CTG TTA GCG TCA CAA GGA TCC CTA	1401
Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser Leu	
435 440 445	
TAC CGG GGT CTG TGG GAT ATT CAG GAA AAC CTA ACG CTT CCG GAA CGG	1449
Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu Arg	
450 455 460 465	
CCT GAG CAG TCA ACC GGA TCT CAG CAT GCA TAGACGTCTG ACTAGAGATT	1499
Pro Glu Gln Ser Thr Gly Ser Gln His Ala	
470 475	
ATATAATAAC CCTCGAGCCA AAATTATACG GCGCTAACAA GTAAAAATTT TAGTTACTTT	1559
TCTGACTTCT CTACGCTGAC TTCTCTACCC TTCTAACATA GTTAATTGAA GTAGTGGTTA	1619
ATGACGACTG CATTTTATTA TTGTCCACTT TGCATTAGAA GTACTAGTGC TTAAGCGCTC	1679
TTTAGGCCGC TTTCTTCTTC TTTGTCAGGC CGCAAGGTAA AGGAAGCACC AACGGATTGC	1739
TACCGCTGCT ATTCCTGCTC TCTCAAG ATG TGT GGC ATA TTA GGC GTT GTG	1790
Met Cys Gly Ile Leu Gly Val Val	
1 5	
CTA GCC GAT CAG TCG AAG GTG GTC GCC CCT GAG TTG TTT GAT GGC TCA	1838
Leu Ala Asp Gln Ser Lys Val Val Ala Pro Glu Leu Phe Asp Gly Ser	
10 15 20	

CTG	TTC	TTA	CAG	CAT	CGC	GGT	CAA	GAT	GCT	GCC	GGG	ATT	GCT	ACG	TGC	1886
Leu	Phe	Leu	Gln	His	Arg	Gly	Gln	Asp	Ala	Ala	Gly	Ile	Ala	Thr	Cys	
25					30					35					40	
GGC	CCC	GGT	GGG	CGC	TTG	TAC	CAA	TGT	AAG	GGC	AAT	GGT	ATG	GCA	CGG	1934
Gly	Pro	Gly	Gly	Arg	Leu	Tyr	Gln	Cys	Lys	Gly	Asn	Gly	Met	Ala	Arg	
				45					50					55		
GAC	GTG	TTC	ACG	CAA	GCT	CGG	ATG	TCA	GGG	TTG	GTT	GGC	TCT	ATG	GGG	1982
Asp	Val	Phe	Thr	Gln	Ala	Arg	Met	Ser	Gly	Leu	Val	Gly	Ser	Met	Gly	
			60					65					70			
ATT	GCA	CAC	CTG	AGA	TAT	CCC	ACT	GCA	GGC	TCC	AGT	GCG	AAC	TCA	GAA	2030
Ile	Ala	His	Leu	Arg	Tyr	Pro	Thr	Ala	Gly	Ser	Ser	Ala	Asn	Ser	Glu	
		75					80					85				
GCG	CAG	CCA	TTC	TAT	GTG	AAT	AGT	CCC	TAC	GGA	ATT	TGC	ATG	AGT	CAT	2078
Ala	Gln	Pro	Phe	Tyr	Val	Asn	Ser	Pro	Tyr	Gly	Ile	Cys	Met	Ser	His	
	90					95					100					
AAT	GGT	AAT	CTG	GTG	AAC	ACG	ATG	TCT	CTA	CGT	AGA	TAT	CTT	GAT	GAA	2126
Asn	Gly	Asn	Leu	Val	Asn	Thr	Met	Ser	Leu	Arg	Arg	Tyr	Leu	Asp	Glu	
105					110					115					120	
GAC	GTT	CAC	CGT	CAT	ATT	AAC	ACG	GAC	AGC	GAT	TCT	GAG	CTA	CTG	CTT	2174
Asp	Val	His	Arg	His	Ile	Asn	Thr	Asp	Ser	Asp	Ser	Glu	Leu	Leu	Leu	
				125				130					135			
AAT	ATA	TTT	GCC	GCG	GAG	CTG	GAA	AAG	TAC	AAC	AAA	TAT	CGT	GTG	AAC	2222
Asn	Ile	Phe	Ala	Ala	Glu	Leu	Glu	Lys	Tyr	Asn	Lys	Tyr	Arg	Val	Asn	
			140					145					150			
AAC	GAT	GAT	ATA	TTT	TGT	GCT	CTA	GAG	GGT	GTT	TAC	AAA	CGT	TGT	CGC	2270
Asn	Asp	Asp	Ile	Phe	Cys	Ala	Leu	Glu	Gly	Val	Tyr	Lys	Arg	Cys	Arg	
		155					160					165				
GGT	GGC	TAT	GCT	TGT	GTT	GGC	ATG	TTG	GCG	GGA	TAT	GGA	TTG	TTT	GGT	2318
Gly	Gly	Tyr	Ala	Cys	Val	Gly	Met	Leu	Ala	Gly	Tyr	Gly	Leu	Phe	Gly	
	170					175					180					
TTC	CGG	GAC	CCC	AAT	GGG	ATC	AGG	CCG	CTA	TTG	TTT	GGT	GAG	CGC	GTC	2366
Phe	Arg	Asp	Pro	Asn	Gly	Ile	Arg	Pro	Leu	Leu	Phe	Gly	Glu	Arg	Val	
185					190					195					200	
AAC	GAT	GAC	GGC	ACC	ATG	GAC	TAC	ATG	CTA	GCG	TCC	GAA	AGT	GTC	GTT	2414
Asn	Asp	Asp	Gly	Thr	Met	Asp	Tyr	Met	Leu	Ala	Ser	Glu	Ser	Val	Val	
				205					210					215		
CTT	AAG	GCC	CAC	CGC	TTC	CAA	AAC	ATA	CGT	GAT	ATT	CTT	CCC	GGC	CAA	2462
Leu	Lys	Ala	His	Arg	Phe	Gln	Asn	Ile	Arg	Asp	Ile	Leu	Pro	Gly	Gln	
			220					225					230			
GCC	GTC	ATT	ATC	CCT	AAA	ACG	TGC	GGC	TCC	AGT	CCA	CCA	GAG	TTC	CGG	2510
Ala	Val	Ile	Ile	Pro	Lys	Thr	Cys	Gly	Ser	Ser	Pro	Pro	Glu	Phe	Arg	
		235					240					245				
CAG	GTA	GTG	CCA	ATT	GAG	GCC	TAC	AAA	CCG	GAC	TTG	TTT	GAG	TAC	GTG	2558
Gln	Val	Val	Pro	Ile	Glu	Ala	Tyr	Lys	Pro	Asp	Leu	Phe	Glu	Tyr	Val	
	250					255					260					

TAT	TTC	GCT	CGT	GCT	GAC	AGC	GTT	CTG	GAC	GGT	ATT	TCC	GTT	TAC	CAT	2606
Tyr	Phe	Ala	Arg	Ala	Asp	Ser	Val	Leu	Asp	Gly	Ile	Ser	Val	Tyr	His	
265					270					275					280	
ACA	CGC	CTG	TTG	ATG	GGT	ATC	AAA	CTT	GCC	GAG	AAC	ATC	AAA	AAA	CAG	2654
Thr	Arg	Leu	Leu	Met	Gly	Ile	Lys	Leu	Ala	Glu	Asn	Ile	Lys	Lys	Gln	
				285					290					295		
ATC	GAT	CTG	GAC	GAA	ATT	GAC	GTT	GTT	GTA	TCT	GTT	CCT	GAC	ACT	GCA	2702
Ile	Asp	Leu	Asp	Glu	Ile	Asp	Val	Val	Val	Ser	Val	Pro	Asp	Thr	Ala	
			300					305					310			
CGT	ACC	TGT	GCA	TTG	GAG	TGT	GCC	AAC	CAT	TTA	AAC	AAA	CCT	TAT	CGC	2750
Arg	Thr	Cys	Ala	Leu	Glu	Cys	Ala	Asn	His	Leu	Asn	Lys	Pro	Tyr	Arg	
		315					320					325				
GAA	GGA	TTT	GTC	AAG	AAC	AGA	TAT	GTT	GGA	AGA	ACA	TTT	ATC	ATG	CCA	2798
Glu	Gly	Phe	Val	Lys	Asn	Arg	Tyr	Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	
	330					335					340					
AAC	CAA	AAA	GAG	CGA	GTA	TCT	TCT	GTG	CGC	CGC	AAG	TTG	AAC	CCA	ATG	2846
Asn	Gln	Lys	Glu	Arg	Val	Ser	Ser	Val	Arg	Arg	Lys	Leu	Asn	Pro	Met	
	345				350					355					360	
AAC	TCA	GAA	TTT	AAA	GAC	AAG	CGC	GTG	CTG	ATT	GTC	GAT	GAT	TCC	ATT	2894
Asn	Ser	Glu	Phe	Lys	Asp	Lys	Arg	Val	Leu	Ile	Val	Asp	Asp	Ser	Ile	
				365					370					375		
GTG	CGA	GGT	ACC	ACT	TCC	AAA	GAG	ATT	GTT	AAC	ATG	GCG	AAG	GAA	TCC	2942
Val	Arg	Gly	Thr	Thr	Ser	Lys	Glu	Ile	Val	Asn	Met	Ala	Lys	Glu	Ser	
			380					385					390			
GGT	GCT	GCC	AAG	GTC	TAC	TTT	GCC	TCT	GCA	GCG	CCA	GCA	ATT	CGT	TTC	2990
Gly	Ala	Ala	Lys	Val	Tyr	Phe	Ala	Ser	Ala	Ala	Pro	Ala	Ile	Arg	Phe	
		395					400					405				
AAT	CAC	ATC	TAC	GGG	ATT	GAC	CTA	GCA	GAT	ACT	AAG	CAG	CTT	GTC	GCC	3038
Asn	His	Ile	Tyr	Gly	Ile	Asp	Leu	Ala	Asp	Thr	Lys	Gln	Leu	Val	Ala	
	410					415					420					
TAC	AAC	AGA	ACT	GTT	GAA	GAA	ATC	ACT	GCG	GAG	CTG	GGC	TGT	GAC	CGC	3086
Tyr	Asn	Arg	Thr	Val	Glu	Glu	Ile	Thr	Ala	Glu	Leu	Gly	Cys	Asp	Arg	
	425				430					435					440	
GTC	ATC	TAT	CAA	TCT	TTG	GAT	GAC	CTC	ATC	GAC	TGT	TGC	AAG	ACA	GAC	3134
Val	Ile	Tyr	Gln	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Cys	Cys	Lys	Thr	Asp	
				445					450					455		
ATC	ATC	TCA	GAA	TTT	GAA	GTT	GGA	GTT	TTC	ACT	GGT	AAC	TAC	GTT	ACA	3182
Ile	Ile	Ser	Glu	Phe	Glu	Val	Gly	Val	Phe	Thr	Gly	Asn	Tyr	Val	Thr	
			460					465					470			
GGT	GTT	GAG	GAT	GTG	TAC	TTG	CAG	GAA	TTA	GAA	CGT	TGC	CGC	GCT	CTT	3230
Gly	Val	Glu	Asp	Val	Tyr	Leu	Gln	Glu	Leu	Glu	Arg	Cys	Arg	Ala	Leu	
		475					480					485				
AAT	AAC	TCG	AAT	AAG	GGT	GAA	GCG	AAG	GCC	GAG	GTT	GAT	ATT	GGT	CTC	3278
Asn	Asn	Ser	Asn	Lys	Gly	Glu	Ala	Lys	Ala	Glu	Val	Asp	Ile	Gly	Leu	
	490					495					500					



TAC AAT TCT GCC GAC TAT TAGCGGCGCC GTTGCCGGCA TCCGGCCCCA	3326
Tyr Asn Ser Ala Asp Tyr	
505 510	
TATATAGACT CATCGGGACC TAAAATAAGC CTTTACAGAT CATTATCTAC AAATATAGAT	3386
ACCATTAATA GCCTGACTTT CGACTTACTC CTAGCACACC CCGTTGTATC CCTGTGCTTG	3446
CTTTCTTAAA TGCCGTTGGT TAGGCTTTGG ACTTAGCGTC CCGCCCATTT TCTAGCATGT	3506
GCAGATCTAG CAAATTTGGC CTAAGACAAG AAGATCCATT CGGCACCCAC ATCCTGGAGC	3566
CAGCACACAG TGGACCCAGA C ATG AGC AGC GGC AAT ATA TGG AAG CAA TTG	3617
Met Ser Ser Gly Asn Ile Trp Lys Gln Leu	
1 5 10	
CTA GAG GAG AAT AGC GAA CAG CTG GAC CAG TCC ACT ACG GAG ACT TAC	3665
Leu Glu Glu Asn Ser Glu Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr	
15 20 25	
GTG GTA TGC TGC GAG AAC GAA GAT TCC CTT AAC CAG TTT TTG CAA CAA	3713
Val Val Cys Cys Glu Asn Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln	
30 35 40	
TGT TGG CAG ATT GAC GAG GGC GAG AAG GTG ACC AAC CTG GAG CCG TTG	3761
Cys Trp Gln Ile Asp Glu Gly Glu Lys Val Thr Asn Leu Glu Pro Leu	
45 50 55	
GGA TTC TTT ACA AAG GTG GTT TCG CGC GAC GAA GAG AAC CTC CGG CTC	3809
Gly Phe Phe Thr Lys Val Val Ser Arg Asp Glu Glu Asn Leu Arg Leu	
60 65 70	
AAC GTA TAC TAT GCC AAG AGC CCA CTG GAT GCA CAG ACG CTG CAG TTT	3857
Asn Val Tyr Tyr Ala Lys Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe	
75 80 85 90	
CTG GGC GTG TTC CTG CGC CAA ATG GAA ACC TCA CAA ATA CGT TGG ATC	3905
Leu Gly Val Phe Leu Arg Gln Met Glu Thr Ser Gln Ile Arg Trp Ile	
95 100 105	
TTC CTA CTG GAC TGG CTG CTA GAC GAT AAA CGA TTA TGG CTA CGT CAA	3953
Phe Leu Leu Asp Trp Leu Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln	
110 115 120	
CTG CGG AAC TCG TGG GCC GCC TTG GAG GAA GCG CAG GTG GCA CCC TTT	4001
Leu Arg Asn Ser Trp Ala Ala Leu Glu Glu Ala Gln Val Ala Pro Phe	
125 130 135	
CCA GGT GGC GCT GTG GTG GTG GTC CTC AAC CCG AGT CAC GTG ACA CAA	4049
Pro Gly Gly Ala Val Val Val Val Leu Asn Pro Ser His Val Thr Gln	
140 145 150	
CTG GAG CGA AAC ACG ATG GTT TGG AAC TCC CGC CGT CTG GAC CTG GTA	4097
Leu Glu Arg Asn Thr Met Val Trp Asn Ser Arg Arg Leu Asp Leu Val	
155 160 165 170	
CAC CAG ACA CTG CGA GCT GCA TGC CTC AAC ACC GGC TCG GCG CTA GTT	4145
His Gln Thr Leu Arg Ala Ala Cys Leu Asn Thr Gly Ser Ala Leu Val	
175 180 185	

ACA CTT GAT CCT AAT ACT GCG CGC GAA GAC GTC ATG CAC ATA TGT GCG	4193
Thr Leu Asp Pro Asn Thr Ala Arg Glu Asp Val Met His Ile Cys Ala	
190 195 200	
CTG CTT GCG GGG CTG CCT ACA TCC CGT CCC GTC GCG ATG CTA AGC CTG	4241
Leu Leu Ala Gly Leu Pro Thr Ser Arg Pro Val Ala Met Leu Ser Leu	
205 210 215	
CAA AGT CTA TTC ATC CCC CAC GGT GCA GAT TCC ATC GGC AAG ATC TGC	4289
Gln Ser Leu Phe Ile Pro His Gly Ala Asp Ser Ile Gly Lys Ile Cys	
220 225 230	
ACC ATC GCG CCC GAG TTC CCT GTT GCT ACG GTG TTC GAC AAC GAT TTT	4337
Thr Ile Ala Pro Glu Phe Pro Val Ala Thr Val Phe Asp Asn Asp Phe	
235 240 245 250	
GTG AGC TCG ACA TTC GAG GCC GCA ATT GCT CCA GAA CTT ACT CCA GGA	4385
Val Ser Ser Thr Phe Glu Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly	
255 260 265	
CCA CGT GTG CCA TCT GAC CAC CCA TGG CTA ACA GAG CCT ACC AAC CCC	4433
Pro Arg Val Pro Ser Asp His Pro Trp Leu Thr Glu Pro Thr Asn Pro	
270 275 280	
CCT TCG GAG GCA ACC GCT TGG CAT TTC GAT CTC CAA GGT CGC CTC GCT	4481
Pro Ser Glu Ala Thr Ala Trp His Phe Asp Leu Gln Gly Arg Leu Ala	
285 290 295	
ACC CTA TAC CGG CAT CTT GGT GAC TCT AAC AAG GCC ATA TCT GTT ACT	4529
Thr Leu Tyr Arg His Leu Gly Asp Ser Asn Lys Ala Ile Ser Val Thr	
300 305 310	
CAG CAC CGC TTC CAC AAG CCC CGC TCG GAA GAT TAT GCA TAC GAA TTC	4577
Gln His Arg Phe His Lys Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe	
315 320 325 330	
GAG CTG CCG TCT AAG CAC CCT ACA ATA CGT GAC CTC ATA CGC TCT GCC	4625
Glu Leu Pro Ser Lys His Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala	
335 340 345	
GCA GCC GAC TCA CCG AAC GAC GTC GCT GAC TCC ATC GAT GGG CTT ATG	4673
Ala Ala Asp Ser Pro Asn Asp Val Ala Asp Ser Ile Asp Gly Leu Met	
350 355 360	
GAT GGT ATC GTA CAA AGG AAT GTT CAT TGACGTCGAC ACAAAAAATTT	4720
Asp Gly Ile Val Gln Arg Asn Val His	
365 370	
TGTTACTGTT CTCTCGAGAA CTATTCTCAT CCAGTACTGA CATATTAGAA GGCGAAGTGA	4780
ACTAGGATTT ATATAAAGTA GCCTTCAGGC AATTGCACAG GGTCTATTGA GTCGCTGCCG	4840
TTCACGAGAG AGCCCAATAT ATCGAGGACT AATTGGTCAC TTTTGTTTTG CTATACTCAC	4900
CCTGTATTTG CTAATCATTT ATCCGCTTTG TCCAAGTGGT TGCGAAGATA TCGAGCCAGA	4960
ACATTAGAAT CTGGTTTGCC GCATCCTAGA GCTGTCTCCA AGCCAGTTGA ACCGTTGCGG	5020
GAGATTACCG CAGCCGGTTT GATCAGAGTA CTGGTGACTG CCAGCACCCA CGTTTGTGAC	5080

TTATAAATAT ACGCCCTGTG GAGCCATAGC CATTGGCATA AAGAGAAGAG CACCCCGTGC 5140  
CACGATGCAG ACACTTCCGG TGTACCCAGC GTCACAGACT GCGTCGCCTA CGAAGCGTGA 5200  
ACTTGCAGCG GCGCCCTCGG TGCCGCAGGA CGGCGCCCGG CTGCCTGCGC AGCTCACTTT 5260  
AGTGACGCCC CCAGAACCTG ATATCCAGAA GAAGTCAGTG CGATCTCAGG TCGCGCGTTT 5320  
AAGCATCTCG GAGACAGATG TAGTGAAGAG TGATATCGTG GCTAAGCTT 5369

<210> 4  
<211> 475  
<212> PRT  
<213> Ashbya gossypii

<400> 4

Met Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val  
1 5 10 15  
Phe His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile  
20 25 30  
Leu Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr  
35 40 45  
Met Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr  
50 55 60  
Arg Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val  
65 70 75 80  
Ala Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn  
85 90 95  
Glu Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg  
100 105 110  
Asp Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly  
115 120 125  
Gln Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala  
130 135 140  
Cys Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu  
145 150 155 160  
Ile Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly  
165 170 175  
Ser Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu  
180 185 190  
Phe Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala  
195 200 205  
Gln Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val  
210 215 220

Thr Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe  
 225 230 235 240  
 Thr Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser  
 245 250 255  
 Gly Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu  
 260 265 270  
 Gln Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu  
 275 280 285  
 Leu Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu  
 290 295 300  
 Phe Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser  
 305 310 315 320  
 Ser Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys  
 325 330 335  
 Leu Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg  
 340 345 350  
 Gly Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg  
 355 360 365  
 Val Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser  
 370 375 380  
 Ala Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln  
 385 390 395 400  
 Asn Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu  
 405 410 415  
 Arg Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser  
 420 425 430  
 Val Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser  
 435 440 445  
 Leu Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu  
 450 455 460  
 Arg Pro Glu Gln Ser Thr Gly Ser Gln His Ala  
 465 470 475

<210> 5  
 <211> 510  
 <212> PRT  
 <213> Ashbya gossypii

<400> 5

Met Cys Gly Ile Leu Gly Val Val Leu Ala Asp Gln Ser Lys Val Val  
 1 5 10 15  
 Ala Pro Glu Leu Phe Asp Gly Ser Leu Phe Leu Gln His Arg Gly Gln

20					25					30					
Asp	Ala	Ala	Gly	Ile	Ala	Thr	Cys	Gly	Pro	Gly	Gly	Arg	Leu	Tyr	Gln
	35						40					45			
Cys	Lys	Gly	Asn	Gly	Met	Ala	Arg	Asp	Val	Phe	Thr	Gln	Ala	Arg	Met
	50					55					60				
Ser	Gly	Leu	Val	Gly	Ser	Met	Gly	Ile	Ala	His	Leu	Arg	Tyr	Pro	Thr
	65					70					75				80
Ala	Gly	Ser	Ser	Ala	Asn	Ser	Glu	Ala	Gln	Pro	Phe	Tyr	Val	Asn	Ser
				85					90					95	
Pro	Tyr	Gly	Ile	Cys	Met	Ser	His	Asn	Gly	Asn	Leu	Val	Asn	Thr	Met
			100					105					110		
Ser	Leu	Arg	Arg	Tyr	Leu	Asp	Glu	Asp	Val	His	Arg	His	Ile	Asn	Thr
		115					120					125			
Asp	Ser	Asp	Ser	Glu	Leu	Leu	Leu	Asn	Ile	Phe	Ala	Ala	Glu	Leu	Glu
	130					135					140				
Lys	Tyr	Asn	Lys	Tyr	Arg	Val	Asn	Asn	Asp	Asp	Ile	Phe	Cys	Ala	Leu
	145					150					155				160
Glu	Gly	Val	Tyr	Lys	Arg	Cys	Arg	Gly	Gly	Tyr	Ala	Cys	Val	Gly	Met
				165					170					175	
Leu	Ala	Gly	Tyr	Gly	Leu	Phe	Gly	Phe	Arg	Asp	Pro	Asn	Gly	Ile	Arg
			180					185					190		
Pro	Leu	Leu	Phe	Gly	Glu	Arg	Val	Asn	Asp	Asp	Gly	Thr	Met	Asp	Tyr
		195					200					205			
Met	Leu	Ala	Ser	Glu	Ser	Val	Val	Leu	Lys	Ala	His	Arg	Phe	Gln	Asn
	210					215					220				
Ile	Arg	Asp	Ile	Leu	Pro	Gly	Gln	Ala	Val	Ile	Ile	Pro	Lys	Thr	Cys
	225					230					235				240
Gly	Ser	Ser	Pro	Pro	Glu	Phe	Arg	Gln	Val	Val	Pro	Ile	Glu	Ala	Tyr
				245					250					255	
Lys	Pro	Asp	Leu	Phe	Glu	Tyr	Val	Tyr	Phe	Ala	Arg	Ala	Asp	Ser	Val
			260					265					270		
Leu	Asp	Gly	Ile	Ser	Val	Tyr	His	Thr	Arg	Leu	Leu	Met	Gly	Ile	Lys
		275					280					285			
Leu	Ala	Glu	Asn	Ile	Lys	Lys	Gln	Ile	Asp	Leu	Asp	Glu	Ile	Asp	Val
	290					295					300				
Val	Val	Ser	Val	Pro	Asp	Thr	Ala	Arg	Thr	Cys	Ala	Leu	Glu	Cys	Ala
	305					310					315				320
Asn	His	Leu	Asn	Lys	Pro	Tyr	Arg	Glu	Gly	Phe	Val	Lys	Asn	Arg	Tyr
				325					330					335	
Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	Asn	Gln	Lys	Glu	Arg	Val	Ser	Ser

340	345	350
Val Arg Arg Lys Leu Asn Pro Met Asn Ser Glu Phe Lys Asp Lys Arg 355 360 365		
Val Leu Ile Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Lys Glu 370 375 380		
Ile Val Asn Met Ala Lys Glu Ser Gly Ala Ala Lys Val Tyr Phe Ala 385 390 395 400		
Ser Ala Ala Pro Ala Ile Arg Phe Asn His Ile Tyr Gly Ile Asp Leu 405 410 415		
Ala Asp Thr Lys Gln Leu Val Ala Tyr Asn Arg Thr Val Glu Glu Ile 420 425 430		
Thr Ala Glu Leu Gly Cys Asp Arg Val Ile Tyr Gln Ser Leu Asp Asp 435 440 445		
Leu Ile Asp Cys Cys Lys Thr Asp Ile Ile Ser Glu Phe Glu Val Gly 450 455 460		
Val Phe Thr Gly Asn Tyr Val Thr Gly Val Glu Asp Val Tyr Leu Gln 465 470 475 480		
Glu Leu Glu Arg Cys Arg Ala Leu Asn Asn Ser Asn Lys Gly Glu Ala 485 490 495		
Lys Ala Glu Val Asp Ile Gly Leu Tyr Asn Ser Ala Asp Tyr 500 505 510		

<210> 6  
 <211> 371  
 <212> PRT  
 <213> Ashbya gossypii

<400> 6

Met Ser Ser Gly Asn Ile Trp Lys Gln Leu Leu Glu Glu Asn Ser Glu 1 5 10 15
Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr Val Val Cys Cys Glu Asn 20 25 30
Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln Cys Trp Gln Ile Asp Glu 35 40 45
Gly Glu Lys Val Thr Asn Leu Glu Pro Leu Gly Phe Phe Thr Lys Val 50 55 60
Val Ser Arg Asp Glu Glu Asn Leu Arg Leu Asn Val Tyr Tyr Ala Lys 65 70 75 80
Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe Leu Gly Val Phe Leu Arg 85 90 95
Gln Met Glu Thr Ser Gln Ile Arg Trp Ile Phe Leu Leu Asp Trp Leu 100 105 110

Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln Leu Arg Asn Ser Trp Ala  
 115 120 125  
 Ala Leu Glu Glu Ala Gln Val Ala Pro Phe Pro Gly Gly Ala Val Val  
 130 135 140  
 Val Val Leu Asn Pro Ser His Val Thr Gln Leu Glu Arg Asn Thr Met  
 145 150 155 160  
 Val Trp Asn Ser Arg Arg Leu Asp Leu Val His Gln Thr Leu Arg Ala  
 165 170 175  
 Ala Cys Leu Asn Thr Gly Ser Ala Leu Val Thr Leu Asp Pro Asn Thr  
 180 185 190  
 Ala Arg Glu Asp Val Met His Ile Cys Ala Leu Leu Ala Gly Leu Pro  
 195 200 205  
 Thr Ser Arg Pro Val Ala Met Leu Ser Leu Gln Ser Leu Phe Ile Pro  
 210 215 220  
 His Gly Ala Asp Ser Ile Gly Lys Ile Cys Thr Ile Ala Pro Glu Phe  
 225 230 235 240  
 Pro Val Ala Thr Val Phe Asp Asn Asp Phe Val Ser Ser Thr Phe Glu  
 245 250 255  
 Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly Pro Arg Val Pro Ser Asp  
 260 265 270  
 His Pro Trp Leu Thr Glu Pro Thr Asn Pro Pro Ser Glu Ala Thr Ala  
 275 280 285  
 Trp His Phe Asp Leu Gln Gly Arg Leu Ala Thr Leu Tyr Arg His Leu  
 290 295 300  
 Gly Asp Ser Asn Lys Ala Ile Ser Val Thr Gln His Arg Phe His Lys  
 305 310 315 320  
 Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe Glu Leu Pro Ser Lys His  
 325 330 335  
 Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala Ala Ala Asp Ser Pro Asn  
 340 345 350  
 Asp Val Ala Asp Ser Ile Asp Gly Leu Met Asp Gly Ile Val Gln Arg  
 355 360 365  
 Asn Val His  
 370

<210> 7

<211> 3616

<212> DNA

<213> *Ashbya gossypii*

<400> 7

GGGCCCCGGTG CCAGCTCGCC AGGTGCGGAC TCGCGCTCGG GCTGTGGGCG CTCTACCTGC

TGCTGCTCGG CAGCTGCCTG ACGCGCGCGT ACGAGCTGTC GGATCTCGAA AACCTGGAAT	120
CCGATTACTA CAGCTACGTG CTGGATGTGA ACTTCGCGCT GCTGAGCGCC ATGAGCGCGA	180
CCGGCCTCGC GATGGGCGCC GTGAGCGGCT CCCTCGGGAG CGCGCCGGTG CTCGCGCAGT	240
GGCCGGCAGC GATCTGGGCC GTGCGCTTCC TGCGCGCCGC GGGCTATGTC GCGATAGTCC	300
TAATCCTGCC GTTCCTGTCC GTCGTCGCAT TCCTGCAGCC GCTCTGCGAG CGCGCGCTGG	360
CGCTGTTCCC GTTTGTGCGC GCGTGGGGCA TGGACGGCGT GTTCAACTTC CTGCTGCTCT	420
CCGCCGTGCT CTGGACTGTA TTCCTGGCCG TTCGCCTGCT CCGCGCCGTC TACAGACTGC	480
TGCGCTGGCT GGTCGGTCTT TTGGTCCGCC TGGCACGCCT GCTGCTGCGA GGCGCCCGTC	540
GGACGCCTGC GGCGGCCCCC GAGGAGCCCG TCTAGCGTGC GCGCGTTCTA GGCCCCTGAC	600
AGCTCCTACC TGGTGCTGGC CGCCGGTAGG GCTCGCATCG TGCGGCGCAG GCCCATTGCT	660
TTTTGGCCCC CGCTGGATCA TCGTTTCTTT TACGTGAAAA GTTTGCAGCG ATGAGCTGCA	720
GTATAAATAG GTTTTCTAGA TGCGCCAAAT CCCAGCTGGG TTTACCGGCG TCTGTTCGGG	780
ATAGTTACTT GATGGATGGG TCAACTTGAG AGCTTGGGTT TAGTGTTGAC TCCTTCTCTT	840
CATAGCACGC CGAACAAAGC GCA ATG ACT TAC AGA GAC GCA GCC ACG GCA	890
Met Thr Tyr Arg Asp Ala Ala Thr Ala	
1 5	
CTG GAG CAC CTG GCG ACG TAC GCC GAG AAG GAC GGG CTG TCC GTG GAG	938
Leu Glu His Leu Ala Thr Tyr Ala Glu Lys Asp Gly Leu Ser Val Glu	
10 15 20 25	
CAG TTG ATG GAC TCC AAG ACG CGG GGC GGG TTG ACG TAC AAC GAC TTC	986
Gln Leu Met Asp Ser Lys Thr Arg Gly Gly Leu Thr Tyr Asn Asp Phe	
30 35 40	
CTG GTC TTG CCG GGC AAG ATC GAC TTC CCA TCG TCG GAG GTG GTG CTG	1034
Leu Val Leu Pro Gly Lys Ile Asp Phe Pro Ser Ser Glu Val Val Leu	
45 50 55	
TCG TCG CGC CTG ACC AAG AAG ATC ACC TTG AAC GCG CCG TTT GTG TCG	1082
Ser Ser Arg Leu Thr Lys Lys Ile Thr Leu Asn Ala Pro Phe Val Ser	
60 65 70	
TCG CCG ATG GAC ACG GTG ACG GAG GCC GAC ATG GCG ATC CAC ATG GCG	1130
Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile His Met Ala	
75 80 85	
CTC CTG GGC GGC ATC GGG ATC ATC CAC CAC AAC TGC ACT GCG GAG GAG	1178
Leu Leu Gly Gly Ile Gly Ile Ile His His Asn Cys Thr Ala Glu Glu	
90 95 100 105	
CAG GCG GAG ATG GTG CGC CGG GTC AAG AAG TAC GAA AAC GGG TTC ATC	1226
Gln Ala Glu Met Val Arg Arg Val Lys Lys Tyr Glu Asn Gly Phe Ile	
110 115 120	
AAC GCC CCC GTG GTC GTG GGG CCG GAC GCG ACG GTG GCG GAC GTG CGC	1274
Asn Ala Pro Val Val Val Gly Pro Asp Ala Thr Val Ala Asp Val Arg	



125	130	135	
CGG ATG AAG AAC GAG TTT GGG TTT GCA GGA TTT CCT GTG ACA			1316
Arg Met Lys Asn Glu Phe Gly Phe Ala Gly Phe Pro Val Thr			
140	145	150	
GGTATGTTAG AGTGGCACGC GGGGCTGCAC GCTGGGATGA TGATCATAAA TCAATAACTT			1376
TCGTTCTACT GACTGCGATC AAACGATCGT GTAGACACCT TTTACTCTGA CCGCAGACGT			1436
GCAGCGCCTT TTTGGCAGGA ACATGTACTA ACACATCAGC A GAT GAT GGC AAG			1489
		Asp Asp Gly Lys	
		1	
CCG ACC GGG AAG CTG CAG GGG ATC ATC ACG TCC CGT GAC ATC CAG TTT			1537
Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg Asp Ile Gln Phe			
5	10	15	20
GTC GAG GAC GAG ACC CTG CTT GTG TCT GAG ATC ATG ACC AAG GAC GTC			1585
Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met Thr Lys Asp Val			
	25	30	35
ATC ACT GGG AAG CAG GGC ATC AAC CTC GAG GAG GCG AAC CAG ATC CTG			1633
Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala Asn Gln Ile Leu			
	40	45	50
AAG AAC ACC AAG AAG GGC AAG CTG CCA ATT GTG GAC GAG GCG GGC TGC			1681
Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp Glu Ala Gly Cys			
	55	60	65
CTG GTG TCC ATG CTT TCG AGA ACT GAC TTG ATG AAG AAC CAG TCC TAC			1729
Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys Asn Gln Ser Tyr			
	70	75	80
CCA TTG GCC TCC AAG TCT GCC GAC ACC AAG CAG CTG CTC TGT GGT GCT			1777
Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu Leu Cys Gly Ala			
85	90	95	100
GCG ATC GGC ACC ATC GAC GCG GAC AGG CAG AGA CTG GCG ATG CTG GTC			1825
Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu Ala Met Leu Val			
	105	110	115
GAG GCC GGT CTG GAC GTT GTT GTG CTA GAC TCC TCG CAG GGT AAC TCG			1873
Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser Gln Gly Asn Ser			
	120	125	130
GTC TTC CAG ATC AAC ATG ATC AAG TGG ATC AAG GAG ACC TTC CCA GAC			1921
Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu Thr Phe Pro Asp			
	135	140	145
CTG CAG GTC ATT GCT GGC AAC GTG GTC ACC AGA GAG CAG GCT GCC AGC			1969
Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu Gln Ala Ala Ser			
	150	155	160
TTG ATC CAC GCC GGC GCA GAC GGG TTG CGT ATC GGT ATG GGC TCT GGC			2017
Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly Met Gly Ser Gly			
165	170	175	180
TCC ATC TGT ATC ACT CAG GAG GTG ATG GCC TGT GGT AGA CCA CAG GGT			2065
Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly Arg Pro Gln Gly			

	185	190	195	
ACC GCT GTC TAC AAC GTC ACG CAG TTC GCC AAC CAG TTT GGT GTG CCA	Thr Ala Val Tyr Asn Val Thr Gln Phe Ala Asn Gln Phe Gly Val Pro	2113		
	200	205	210	
TGT ATT GCT GAC GGT GGT GTC CAG AAC ATC GGG CAC ATT ACC AAA GCT	Cys Ile Ala Asp Gly Gly Val Gln Asn Ile Gly His Ile Thr Lys Ala	2161		
	215	220	225	
ATC GCT CTT GGC GCG TCC ACC GTC ATG ATG GGC GGT ATG CTG GCA GGC	Ile Ala Leu Gly Ala Ser Thr Val Met Met Gly Gly Met Leu Ala Gly	2209		
	230	235	240	
ACT ACA GAG TCT CCA GGC GAG TAC TTC TTC AGG GAC GGG AAG AGA CTG	Thr Thr Glu Ser Pro Gly Glu Tyr Phe Phe Arg Asp Gly Lys Arg Leu	2257		
	245	250	255	260
AAG ACC TAC AGA GGT ATG GGC TCC ATC GAC GCC ATG CAA AAG ACT GAT	Lys Thr Tyr Arg Gly Met Gly Ser Ile Asp Ala Met Gln Lys Thr Asp	2305		
	265	270	275	
GTC AAG GGT AAC GCC GCT ACC TCC CGT TAC TTC TCT GAG TCT GAC AAG	Val Lys Gly Asn Ala Ala Thr Ser Arg Tyr Phe Ser Glu Ser Asp Lys	2353		
	280	285	290	
GTT CTG GTC GCT CAG GGT GTT ACT GGT TCT GTG ATC GAC AAG GGC TCC	Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile Asp Lys Gly Ser	2401		
	295	300	305	
ATC AAG AAG TAC ATT CCA TAT CTG TAC AAT GGT CTA CAG CAC TCG TGC	Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu Gln His Ser Cys	2449		
	310	315	320	
CAG GAT ATC GGT GTG CGC TCT CTA GTG GAG TTC AGA GAG AAG GTG GAC	Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg Glu Lys Val Asp	2497		
	325	330	335	340
TCT GGC TCG GTC AGA TTT GAG TTC AGA ACT CCA TCT GCC CAG TTG GAG	Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser Ala Gln Leu Glu	2545		
	345	350	355	
GGT GGT GTG CAC AAC TTG CAC TCC TAC GAG AAG CGC CTA TTT GACTGAGTGC	Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg Leu Phe Asp	2597		
	360	365	370	
CACTAGGCCCC ACACTATAGA AGTGGATCCG GGCGCGATGG CACCCATACT TTTATATTAT		2657		
GTTGATTGAT GTACGTAAAC GATAGATATA ATAACAGACG CGGCATCTCA TTTGTATGCA		2717		
ATATATCTGG AACATGGTTA TGCGTACTCA ACTGTATGTA CTACTTTATA TACACAGCTC		2777		
TGGGACACTT GGTGAGATAT ATGTTTCATT ATGTATGCCT CGCTATCGAA AGGTCTGGCA		2837		
TTATGGGCTA CTGGGTCTAA GAGTCATGGC TTATGAGTAT TTATTTATTT ATTTCTCTTC		2897		
CTTTTCATTA AACTCCTCGA GCTTCTTTCT GTAATACTGC TCTCTAGACT TCTCCACATC		2957		
TGCTAATGAT GGTGGAAGTC GTTCGTTTTT CAAATCCGCT CTACGAGCGC GCTCGAAGTT		3017		

AGACAGCGCC TCGTTCAGAC CTTCAGACCC GCGTGACAGC GCTCCACGAG GCAGCAGGCC 3077  
 AGAATTCATT GTTTTTAGGT ACTGCACCTT ATCGCTCTCT TCTCTCAACA CGCTATACAT 3137  
 TCGGGAAACC TTGGCAATCG CCAATATTTT ACTGCGTAGT GCACGCCGTT TTGCATCATC 3197  
 GTCCAGAATA GACCGTTTTT TCTTCGATTT CTTGGAGCCA GGTATAACAG TTACAACCTG 3257  
 CTCAGTGTTT TTGGACTTCA ATGTAGCACC TAAGTCCTCC CTTATAACAA AAGTCTCTTC 3317  
 CTCCAATTCT TCTTCAGTAC AAATGTTTAA TATCGAAACC AACATTTTCTC TCACTTTCTC 3377  
 GCCAACAAAT GGCAAAGACC AGGTGAATAC GTCCATGAAA TTCGGTAACC AATACGGATG 3437  
 CTGTGACATG TTAAATTGTC TAATGTTTCAT AACGTTATCC GAGTATTTTA GGACCGCGGC 3497  
 CTTGTTCTTG TAAGTGTTCA AGTAGTTGGG TGCCTGAAC AACGTAAGTA AACTAGGAAA 3557  
 GCCCAGATTC TTGGTATTCT TGTACATTCT GTAGCCCTGA TCTTGGGCTT CGTGGGCCC 3616

<210> 8

<211> 151

<212> PRT

<213> Ashbya gossypii

<400> 8

Met Thr Tyr Arg Asp Ala Ala Thr Ala Leu Glu His Leu Ala Thr Tyr  
 1 5 10 15  
 Ala Glu Lys Asp Gly Leu Ser Val Glu Gln Leu Met Asp Ser Lys Thr  
 20 25 30  
 Arg Gly Gly Leu Thr Tyr Asn Asp Phe Leu Val Leu Pro Gly Lys Ile  
 35 40 45  
 Asp Phe Pro Ser Ser Glu Val Val Leu Ser Ser Arg Leu Thr Lys Lys  
 50 55 60  
 Ile Thr Leu Asn Ala Pro Phe Val Ser Ser Pro Met Asp Thr Val Thr  
 65 70 75 80  
 Glu Ala Asp Met Ala Ile His Met Ala Leu Leu Gly Gly Ile Gly Ile  
 85 90 95  
 Ile His His Asn Cys Thr Ala Glu Glu Gln Ala Glu Met Val Arg Arg  
 100 105 110  
 Val Lys Lys Tyr Glu Asn Gly Phe Ile Asn Ala Pro Val Val Val Gly  
 115 120 125  
 Pro Asp Ala Thr Val Ala Asp Val Arg Arg Met Lys Asn Glu Phe Gly  
 130 135 140  
 Phe Ala Gly Phe Pro Val Thr  
 145 150

<210> 9

<211> 371  
<212> PRT  
<213> Ashbya gossypii

<400> 9

Asp	Asp	Gly	Lys	Pro	Thr	Gly	Lys	Leu	Gln	Gly	Ile	Ile	Thr	Ser	Arg	
1				5					10					15		
Asp	Ile	Gln	Phe	Val	Glu	Asp	Glu	Thr	Leu	Leu	Val	Ser	Glu	Ile	Met	
		20						25					30			
Thr	Lys	Asp	Val	Ile	Thr	Gly	Lys	Gln	Gly	Ile	Asn	Leu	Glu	Glu	Ala	
		35					40					45				
Asn	Gln	Ile	Leu	Lys	Asn	Thr	Lys	Lys	Gly	Lys	Leu	Pro	Ile	Val	Asp	
	50					55					60					
Glu	Ala	Gly	Cys	Leu	Val	Ser	Met	Leu	Ser	Arg	Thr	Asp	Leu	Met	Lys	
65					70					75					80	
Asn	Gln	Ser	Tyr	Pro	Leu	Ala	Ser	Lys	Ser	Ala	Asp	Thr	Lys	Gln	Leu	
				85					90					95		
Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	Ile	Asp	Ala	Asp	Arg	Gln	Arg	Leu	
			100					105					110			
Ala	Met	Leu	Val	Glu	Ala	Gly	Leu	Asp	Val	Val	Val	Leu	Asp	Ser	Ser	
		115					120						125			
Gln	Gly	Asn	Ser	Val	Phe	Gln	Ile	Asn	Met	Ile	Lys	Trp	Ile	Lys	Glu	
	130					135					140					
Thr	Phe	Pro	Asp	Leu	Gln	Val	Ile	Ala	Gly	Asn	Val	Val	Thr	Arg	Glu	
145					150					155					160	
Gln	Ala	Ala	Ser	Leu	Ile	His	Ala	Gly	Ala	Asp	Gly	Leu	Arg	Ile	Gly	
				165					170					175		
Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Met	Ala	Cys	Gly	
			180					185					190			
Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Asn	Val	Thr	Gln	Phe	Ala	Asn	Gln	
		195					200					205				
Phe	Gly	Val	Pro	Cys	Ile	Ala	Asp	Gly	Gly	Val	Gln	Asn	Ile	Gly	His	
	210					215					220					
Ile	Thr	Lys	Ala	Ile	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	Gly	
225					230					235					240	
Met	Leu	Ala	Gly	Thr	Thr	Glu	Ser	Pro	Gly	Glu	Tyr	Phe	Phe	Arg	Asp	
				245					250					255		
Gly	Lys	Arg	Leu	Lys	Thr	Tyr	Arg	Gly	Met	Gly	Ser	Ile	Asp	Ala	Met	
			260					265					270			
Gln	Lys	Thr	Asp	Val	Lys	Gly	Asn	Ala	Ala	Thr	Ser	Arg	Tyr	Phe	Ser	
		275					280						285			

Glu Ser Asp Lys Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile  
 290 295 300  
 Asp Lys Gly Ser Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu  
 305 310 315 320  
 Gln His Ser Cys Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg  
 325 330 335  
 Glu Lys Val Asp Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser  
 340 345 350  
 Ala Gln Leu Glu Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg  
 355 360 365  
 Leu Phe Asp  
 370

<210> 10  
 <211> 2697  
 <212> DNA  
 <213> Ashbya gossypii

<400> 10

ATCGATTTCA GGAGATTTTT GGTAGCATTA TTGAGGTCAT TAGAGGCGTT CTGTGACTTT	60
CGACGATTTG CACGCGCAGA AGAGGGCGTT CAACCAGCCT TTCGGATATT CCGGTTTCGAG	120
TTATACCAGC AGGGATCAGC GCAGGCACTA GAGTGGCGGG TGCTAATAAG AGGAGCAGGT	180
CCTGGAAGT AAGTTGCAAG AGATAAGCAT TGC GCGGAGA AGGAGGCGGT TAGAGGGTGC	240
AAGCGAGCAG GATGGGGTCT TCGATGAACT TCCCGTCTGG GTATGTGAAC AAGCACACGC	300
TGCAGGCACA CCGGTAGGGC GAGTGCAGGG TGAAAAATAT ATATGCGCTC GAGAAGCGCT	360
GGGGATGAGT TCGTCTGCAA CGGCAGGCGG ATCTTCATCT GACAAAACCA GCTGCCTACA	420
TCAGTGC GAA GCTGTT CAGT GATAGA ATAG GAGTA ATG GCT GCT GTT GAA CAA	473
Met Ala Ala Val Glu Gln	
1 5	
GTT TCT AGC GTG TTT GAC ACC ATT TTG GTG CTG GAC TTC GGG TCC CAG	521
Val Ser Ser Val Phe Asp Thr Ile Leu Val Leu Asp Phe Gly Ser Gln	
10 15 20	
TAC TCG CAT CTG ATC ACG CGG CGG CTG CGT GAG TTT AAT GTG TAC GCG	569
Tyr Ser His Leu Ile Thr Arg Arg Leu Arg Glu Phe Asn Val Tyr Ala	
25 30 35	
GAG ATG CTT CCG TGT ACG CAG AAG ATC AGC GAG CTG GGC TGG AAG CCA	617
Glu Met Leu Pro Cys Thr Gln Lys Ile Ser Glu Leu Gly Trp Lys Pro	
40 45 50	
AAG GGT GTG ATT TTG TCA GGC GGG CCG TAC TCC GTG TAC GCG GCA GAT	665
Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr Ser Val Tyr Ala Ala Asp	
55 60 65 70	
GCT CCG CAC GTG GAC CGG GCG GTG TTC GAG TTG GGC GTT CCA ATT CTG	713

Ala	Pro	His	Val	Asp	Arg	Ala	Val	Phe	Glu	Leu	Gly	Val	Pro	Ile	Leu	
				75					80					85		
GGC	ATC	TGC	TAC	GGG	CTA	CAG	GAG	CTT	GCG	TGG	ATA	GCC	GGC	GCA	GAG	761
Gly	Ile	Cys	Tyr	Gly	Leu	Gln	Glu	Leu	Ala	Trp	Ile	Ala	Gly	Ala	Glu	
			90					95					100			
GTG	GGG	CGC	GGC	GAG	AAG	CGC	GAG	TAC	GGG	CGC	GCG	ACG	CTG	CAC	GTG	809
Val	Gly	Arg	Gly	Glu	Lys	Arg	Glu	Tyr	Gly	Arg	Ala	Thr	Leu	His	Val	
		105					110					115				
GAG	GAC	AGC	GCG	TGC	CCG	CTG	TTC	AAC	AAC	GTG	GAC	AGC	AGC	ACG	GTG	857
Glu	Asp	Ser	Ala	Cys	Pro	Leu	Phe	Asn	Asn	Val	Asp	Ser	Ser	Thr	Val	
	120					125					130					
TGG	ATG	TCG	CAC	GGT	GAC	AAG	CTG	CAC	GCA	CTA	CCT	GCG	GAT	TTC	CAC	905
Trp	Met	Ser	His	Gly	Asp	Lys	Leu	His	Ala	Leu	Pro	Ala	Asp	Phe	His	
135					140					145					150	
GTC	ACT	GCG	ACG	ACG	GAG	AAC	TCT	CCT	TTC	TGC	GGG	ATT	GCA	CAC	GAC	953
Val	Thr	Ala	Thr	Thr	Glu	Asn	Ser	Pro	Phe	Cys	Gly	Ile	Ala	His	Asp	
				155					160					165		
TCG	AAG	CCA	ATC	TTC	GGG	ATC	CAG	TTC	CAC	CCT	GAG	GTG	ACG	CAC	TCC	1001
Ser	Lys	Pro	Ile	Phe	Gly	Ile	Gln	Phe	His	Pro	Glu	Val	Thr	His	Ser	
			170					175					180			
TCG	CAG	GGG	AAG	ACG	TTG	CTG	AAG	AAC	TTT	GCG	GTG	GAG	ATC	TGC	CAG	1049
Ser	Gln	Gly	Lys	Thr	Leu	Leu	Lys	Asn	Phe	Ala	Val	Glu	Ile	Cys	Gln	
		185					190					195				
GCC	GCG	CAG	ACC	TGG	ACG	ATG	GAA	AAC	TTC	ATT	GAC	ACC	GAG	ATC	CAG	1097
Ala	Ala	Gln	Thr	Trp	Thr	Met	Glu	Asn	Phe	Ile	Asp	Thr	Glu	Ile	Gln	
	200					205					210					
CGG	ATC	CGG	ACC	CTT	GTG	GGC	CCC	ACC	GCG	GAA	GTG	ATC	GGT	GCT	GTG	1145
Arg	Ile	Arg	Thr	Leu	Val	Gly	Pro	Thr	Ala	Glu	Val	Ile	Gly	Ala	Val	
215					220					225					230	
TCC	GGC	GGT	GTC	GAC	TCG	ACC	GTC	GCT	GCG	AAG	CTG	ATG	ACC	GAG	GCC	1193
Ser	Gly	Gly	Val	Asp	Ser	Thr	Val	Ala	Ala	Lys	Leu	Met	Thr	Glu	Ala	
				235					240					245		
ATC	GGC	GAC	CGG	TTC	CAC	GCG	ATC	CTG	GTC	GAC	AAC	GGT	GTT	CTG	CGC	1241
Ile	Gly	Asp	Arg	Phe	His	Ala	Ile	Leu	Val	Asp	Asn	Gly	Val	Leu	Arg	
			250					255					260			
CTC	AAC	GAA	GCG	GCC	AAT	GTG	AAG	AAA	ATC	CTC	GGC	GAG	GGC	TTG	GGC	1289
Leu	Asn	Glu	Ala	Ala	Asn	Val	Lys	Lys	Ile	Leu	Gly	Glu	Gly	Leu	Gly	
		265					270					275				
ATC	AAC	TTG	ACT	GTT	GTT	GAC	GCC	TCC	GAA	GAG	TTC	TTG	ACG	AAG	CTC	1337
Ile	Asn	Leu	Thr	Val	Val	Asp	Ala	Ser	Glu	Glu	Phe	Leu	Thr	Lys	Leu	
	280					285					290					
AAG	GGC	GTC	ACG	GAC	CCT	GAG	AAG	AAG	AGA	AAG	ATC	ATC	GGT	AAC	ACC	1385
Lys	Gly	Val	Thr	Asp	Pro	Glu	Lys	Lys	Arg	Lys	Ile	Ile	Gly	Asn	Thr	
295					300					305					310	
TTC	ATT	CAT	GTT	TTT	GAG	CGC	GAG	GCA	GCC	AGG	ATC	CAG	CCT	AAG	AAC	1433

Phe	Ile	His	Val	Phe	Glu	Arg	Glu	Ala	Ala	Arg	Ile	Gln	Pro	Lys	Asn		
				315					320					325			
GGC	GAG	GAG	ATT	GAG	TTC	CTG	TTG	CAG	GGT	ACC	CTA	TAC	CCT	GAC	GTT	1481	
Gly	Glu	Glu	Ile	Glu	Phe	Leu	Leu	Gln	Gly	Thr	Leu	Tyr	Pro	Asp	Val		
				330					335					340			
ATC	GAG	TCC	ATT	TCC	TTT	AAG	GGC	CCA	TCT	CAG	ACG	ATC	AAG	ACC	CAC	1529	
Ile	Glu	Ser	Ile	Ser	Phe	Lys	Gly	Pro	Ser	Gln	Thr	Ile	Lys	Thr	His		
				345					350					355			
CAT	AAC	GTC	GGT	GGT	CTT	TTG	GAC	AAC	ATG	AAA	CTG	AAG	CTC	ATT	GAG	1577	
His	Asn	Val	Gly	Gly	Leu	Leu	Asp	Asn	Met	Lys	Leu	Lys	Leu	Ile	Glu		
				360					365					370			
CCT	TTG	CGC	GAG	CTT	TTC	AAG	GAC	GAG	GTG	AGA	CAC	CTG	GGA	GAA	CTA	1625	
Pro	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Glu	Val	Arg	His	Leu	Gly	Glu	Leu		
				375					380					385			390
TTG	GGG	ATC	TCC	CAC	GAG	TTG	GTC	TGG	AGA	CAT	CCG	TTC	CCA	GGC	CCA	1673	
Leu	Gly	Ile	Ser	His	Glu	Leu	Val	Trp	Arg	His	Pro	Phe	Pro	Gly	Pro		
				395					400					405			
GGT	ATC	GCC	ATC	CGT	GTG	CTA	GGC	GAG	GTC	ACC	AAG	GAG	CAG	GTG	GAG	1721	
Gly	Ile	Ala	Ile	Arg	Val	Leu	Gly	Glu	Val	Thr	Lys	Glu	Gln	Val	Glu		
				410					415					420			
ATT	GCC	AGA	AAG	GCA	GAC	CAC	ATC	TAC	ATC	GAG	GAG	ATC	AGG	AAA	GCA	1769	
Ile	Ala	Arg	Lys	Ala	Asp	His	Ile	Tyr	Ile	Glu	Glu	Ile	Arg	Lys	Ala		
				425					430					435			
GGT	CTA	TAC	AAC	AAG	ATT	TCT	CAA	GCT	TTT	GCT	TGC	TTG	CTG	CCT	GTT	1817	
Gly	Leu	Tyr	Asn	Lys	Ile	Ser	Gln	Ala	Phe	Ala	Cys	Leu	Leu	Pro	Val		
				440					445					450			
AAG	TCT	GTG	GGT	GTC	ATG	GGT	GAC	CAG	AGA	ACC	TAC	GAC	CAG	GTC	ATT	1865	
Lys	Ser	Val	Gly	Val	Met	Gly	Asp	Gln	Arg	Thr	Tyr	Asp	Gln	Val	Ile		
				455					460					465			470
GCT	CTA	AGA	GCA	ATT	GAG	ACC	ACG	GAC	TTC	ATG	ACT	GCC	GAC	TGG	TAT	1913	
Ala	Leu	Arg	Ala	Ile	Glu	Thr	Thr	Asp	Phe	Met	Thr	Ala	Asp	Trp	Tyr		
				475					480					485			
CCA	TTT	GAG	CAC	GAA	TTC	TTG	AAG	CAT	GTC	GCA	TCC	CGT	ATT	GTT	AAC	1961	
Pro	Phe	Glu	His	Glu	Phe	Leu	Lys	His	Val	Ala	Ser	Arg	Ile	Val	Asn		
				490					495					500			
GAG	GTT	GAA	GGT	GTT	GCC	AGA	GTC	ACC	TAC	GAC	ATA	ACT	TCT	AAG	CCT	2009	
Glu	Val	Glu	Gly	Val	Ala	Arg	Val	Thr	Tyr	Asp	Ile	Thr	Ser	Lys	Pro		
				505					510					515			
CCA	GCT	ACC	GTT	GAA	TGG	GAA	TAATCACCCT	TGGGATCCGC	TGACTGGCTA							2060	
Pro	Ala	Thr	Val	Glu	Trp	Glu											
				520					525								
CTGTAATTCT			ATGTAGTGGA			TTAGTACGAT			AAGTTACTTT			TGTATGATAG			ATGTAATCAC		2120
ATCTGGCTAT			TAAAATGACT			CAGCCGAGGT			AAATCTAACG			TCCCTTCACA			AGGGTGTTC		2180
TGTGTGGACT			TCCGCCTGAA			TTTTTATAGA			TATATAGATA			CTCTACTCAT			GAACAACCTG		2240

CAACCGAATA AGCATTAGTG CCAGGAGAAG AGAACCGTGG AAATGGGGCA AGTAGAAAAA 2300  
 ATCATATTCC TTAAGAATAA GACAGTACCA GAGGACCATT ACGAGACGAT TTTTGAATCG 2360  
 AATGGCTTCC AGACTCACTT TGTACCCATA ATAACCCATG AACACCTGCC AGATGAGGTT 2420  
 CGCGGTGCGAC TATCCGACGC GAATTACATG AAAAGGTTGA ATTGTTTGGT GGTAACCTCT 2480  
 CAGAGGACTG TGGAGTGTCT CTATGAGGAC GTTCTGCCCT CTCTTCCAGC TGAAGCACGC 2540  
 AAATCTCTTC TCAATACGCC AGTATTCTGT GTTGGGCGTG CCACTCAGGA ATTTATGGAG 2600  
 AGATGCGGCT TTACGGACGT GAGAGGGGGA TCTGAGACTG GTAATGGCGT TTTGCTAGCG 2660  
 GAGTTAATGT TAAATATGAT CCAGAAGGGC GATGGGG 2697

<210> 11  
 <211> 525  
 <212> PRT  
 <213> Ashbya gossypii

<400> 11

Met Ala Ala Val Glu Gln Val Ser Ser Val Phe Asp Thr Ile Leu Val  
 1 5 10 15  
 Leu Asp Phe Gly Ser Gln Tyr Ser His Leu Ile Thr Arg Arg Leu Arg  
 20 25 30  
 Glu Phe Asn Val Tyr Ala Glu Met Leu Pro Cys Thr Gln Lys Ile Ser  
 35 40 45  
 Glu Leu Gly Trp Lys Pro Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr  
 50 55 60  
 Ser Val Tyr Ala Ala Asp Ala Pro His Val Asp Arg Ala Val Phe Glu  
 65 70 75 80  
 Leu Gly Val Pro Ile Leu Gly Ile Cys Tyr Gly Leu Gln Glu Leu Ala  
 85 90 95  
 Trp Ile Ala Gly Ala Glu Val Gly Arg Gly Glu Lys Arg Glu Tyr Gly  
 100 105 110  
 Arg Ala Thr Leu His Val Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn  
 115 120 125  
 Val Asp Ser Ser Thr Val Trp Met Ser His Gly Asp Lys Leu His Ala  
 130 135 140  
 Leu Pro Ala Asp Phe His Val Thr Ala Thr Thr Glu Asn Ser Pro Phe  
 145 150 155 160  
 Cys Gly Ile Ala His Asp Ser Lys Pro Ile Phe Gly Ile Gln Phe His  
 165 170 175  
 Pro Glu Val Thr His Ser Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe  
 180 185 190



Ala	Val	Glu	Ile	Cys	Gln	Ala	Ala	Gln	Thr	Trp	Thr	Met	Glu	Asn	Phe	195	200	205	
Ile	Asp	Thr	Glu	Ile	Gln	Arg	Ile	Arg	Thr	Leu	Val	Gly	Pro	Thr	Ala	210	215	220	
Glu	Val	Ile	Gly	Ala	Val	Ser	Gly	Gly	Val	Asp	Ser	Thr	Val	Ala	Ala	225	230	235	240
Lys	Leu	Met	Thr	Glu	Ala	Ile	Gly	Asp	Arg	Phe	His	Ala	Ile	Leu	Val	245	250	255	
Asp	Asn	Gly	Val	Leu	Arg	Leu	Asn	Glu	Ala	Ala	Asn	Val	Lys	Lys	Ile	260	265	270	
Leu	Gly	Glu	Gly	Leu	Gly	Ile	Asn	Leu	Thr	Val	Val	Asp	Ala	Ser	Glu	275	280	285	
Glu	Phe	Leu	Thr	Lys	Leu	Lys	Gly	Val	Thr	Asp	Pro	Glu	Lys	Lys	Arg	290	295	300	
Lys	Ile	Ile	Gly	Asn	Thr	Phe	Ile	His	Val	Phe	Glu	Arg	Glu	Ala	Ala	305	310	315	320
Arg	Ile	Gln	Pro	Lys	Asn	Gly	Glu	Glu	Ile	Glu	Phe	Leu	Leu	Gln	Gly	325	330	335	
Thr	Leu	Tyr	Pro	Asp	Val	Ile	Glu	Ser	Ile	Ser	Phe	Lys	Gly	Pro	Ser	340	345	350	
Gln	Thr	Ile	Lys	Thr	His	His	Asn	Val	Gly	Gly	Leu	Leu	Asp	Asn	Met	355	360	365	
Lys	Leu	Lys	Leu	Ile	Glu	Pro	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Glu	Val	370	375	380	
Arg	His	Leu	Gly	Glu	Leu	Leu	Gly	Ile	Ser	His	Glu	Leu	Val	Trp	Arg	385	390	395	400
His	Pro	Phe	Pro	Gly	Pro	Gly	Ile	Ala	Ile	Arg	Val	Leu	Gly	Glu	Val	405	410	415	
Thr	Lys	Glu	Gln	Val	Glu	Ile	Ala	Arg	Lys	Ala	Asp	His	Ile	Tyr	Ile	420	425	430	
Glu	Glu	Ile	Arg	Lys	Ala	Gly	Leu	Tyr	Asn	Lys	Ile	Ser	Gln	Ala	Phe	435	440	445	
Ala	Cys	Leu	Leu	Pro	Val	Lys	Ser	Val	Gly	Val	Met	Gly	Asp	Gln	Arg	450	455	460	
Thr	Tyr	Asp	Gln	Val	Ile	Ala	Leu	Arg	Ala	Ile	Glu	Thr	Thr	Asp	Phe	465	470	475	480
Met	Thr	Ala	Asp	Trp	Tyr	Pro	Phe	Glu	His	Glu	Phe	Leu	Lys	His	Val	485	490	495	
Ala	Ser	Arg	Ile	Val	Asn	Glu	Val	Glu	Gly	Val	Ala	Arg	Val	Thr	Tyr	500	505	510	

Asp Ile Thr Ser Lys Pro Pro Ala Thr Val Glu Trp Glu  
 515 520 525

<210> 12  
 <211> 1634  
 <212> DNA  
 <213> Ashbya gossypii

<400> 12

CCTCGAACAT CTATCTTCTG AGCTCGATAG TCTACGAAAT CGGCACACTA GCCTAATTGC	60
CGAGATGAAG AGCTCCAGGG AACCGTTAAA GATCTGATGT TCCATCTTCA ATCAGGACAA	120
ATGTTACGGG ATGTCCCTGA CGCCACAGAA GGTAGCCTGG TGGTCCAGAC AGAAAAAGAG	180
CCTACACCAA AGAAGAAACA TAACAAGAAA AAGCCTCCGC ATCGTTTTGG TAAATCATAA	240
TAGGCACGAT GCGCATATAC CCTGACCATC ATAGCGGTTC CCCCCGCTAA CTGCTCCGAG	300
CGGGTAACCC CATGTCACAA AGTGACTCTG TCTCTTCGTG GTAGGTGATG TCAAATTTTC	360
ACGACTTCCC ACCCCGATGA GCATCCGTAT TCCTTTTCAT CTAAATTCTA ATAGATGGCT	420
TATGGATTCT TATTGGCGAC TTACAAGCCT ATGTAGTTGG CTTCCCTCAA GTGTTCGTAG	480
TCTACCACCT CACACCCGGT CTAACAGCTT ACGAGAATA ATG GCT ACT AAT GCA	534
Met Ala Thr Asn Ala	
1 5	
ATC AAG CTT CTT GCG CCA GAT ATC CAC AGG GGT CTG GCA GAG CTG GTC	582
Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly Leu Ala Glu Leu Val	
10 15 20	
GCT AAA CGC CTA GGC TTA CGT CTG ACA GAC TGC AAG CTT AAG CGG GAT	630
Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys Lys Leu Lys Arg Asp	
25 30 35	
TGT AAC GGG GAG GCG ACA TTT TCG ATC GGA GAA TCT GTT CGA GAC CAG	678
Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu Ser Val Arg Asp Gln	
40 45 50	
GAT ATC TAC ATC ATC ACG CAG GTG GGG TCC GGG GAC GTG AAC GAC CGA	726
Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly Asp Val Asn Asp Arg	
55 60 65	
GTG CTG GAG CTG CTC ATC ATG ATC AAC GCT AGC AAG ACG GCG TCT GCG	774
Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser Lys Thr Ala Ser Ala	
70 75 80 85	
CGG CGA ATT ACG GCT GTG ATT CCA AAC TTC CCA TAC GCG CGG CAG GAC	822
Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp	
90 95 100	
CGG AAG GAT AAG TCA CGG GCG CCA ATT ACC GCG AAG CTC ATG GCG GAC	870
Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Met Ala Asp	
105 110 115	
ATG CTG ACT ACC GCG GGC TGC GAT CAT GTC ATC ACC ATG GAC TTA CAC	918
Met Leu Thr Thr Ala Gly Cys Asp His Val Ile Thr Met Asp Leu His	

120	125	130	
GCT TCG CAA ATC CAG GGC TTC TTT GAT GTA CCA GTT GAC AAC CTT TAC			966
Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro Val Asp Asn Leu Tyr			
135	140	145	
GCA GAG CCT AGC GTG GTG AAG TAT ATC AAG GAG CAT ATT CCC CAC GAC			1014
Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu His Ile Pro His Asp			
150	155	160	165
GAT GCC ATC ATC ATC TCG CCG GAT GCT GGT GGT GCC AAA CGT GCG TCG			1062
Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly Ala Lys Arg Ala Ser			
170	175	180	
CTT CTA TCA GAT CGC CTA AAC TTG AAC TTT GCG CTG ATT CAT AAG GAA			1110
Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu			
185	190	195	
CGT GCA AAG GCA AAC GAA GTG TCC CGC ATG GTT CTG GTC GGC GAT GTT			1158
Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val			
200	205	210	
ACC GAT AAA GTC TGC ATT ATC GTT GAC GAT ATG GCG GAT ACT TGT GGT			1206
Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly			
215	220	225	
ACG CTG GCC AAG GCG GCA GAA GTG CTG CTA GAG CAC AAC GCG CGG TCT			1254
Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu His Asn Ala Arg Ser			
230	235	240	245
GTG ATA GCC ATT GTT ACC CAC GGT ATC CTT TCA GGA AAG GCC ATT GAG			1302
Val Ile Ala Ile Val Thr His Gly Ile Leu Ser Gly Lys Ala Ile Glu			
250	255	260	
AAC ATC AAC AAT TCG AAG CTT GAT AGG GTT GTG TGT ACC AAC ACC GTG			1350
Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val Cys Thr Asn Thr Val			
265	270	275	
CCA TTC GAG GAG AAG ATG AAG TTA TGC CCG AAG TTA GAT GTA ATT GAT			1398
Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys Leu Asp Val Ile Asp			
280	285	290	
ATC TCG GCA GTT CTT GCG GAA TCC ATT CGC CGT CTA CAC AAT GGT GAA			1446
Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg Leu His Asn Gly Glu			
295	300	305	
AGT ATC TCC TAC CTC TTT AAA AAC AAC CCA CTA TGATTTTGCT TCTCGATGCT			1499
Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu			
310	315	320	
GGCTTCTTGA GGGCCAATTT TGCCGTAGAG GTAGTATCCC TTCTTTTAT ATTGACTATT			1559
TAACGAAGAC TATTTCTTCA TAAATGGACT TCGGCTTCAC TGTGAATCTC ACATGATATA			1619
GTTGTTTCAG AGACC			1634

<210> 13  
 <211> 320  
 <212> PRT

<213> Ashbya gossypii

<400> 13

Met	Ala	Thr	Asn	Ala	Ile	Lys	Leu	Leu	Ala	Pro	Asp	Ile	His	Arg	Gly
1				5					10					15	
Leu	Ala	Glu	Leu	Val	Ala	Lys	Arg	Leu	Gly	Leu	Arg	Leu	Thr	Asp	Cys
			20					25					30		
Lys	Leu	Lys	Arg	Asp	Cys	Asn	Gly	Glu	Ala	Thr	Phe	Ser	Ile	Gly	Glu
		35					40					45			
Ser	Val	Arg	Asp	Gln	Asp	Ile	Tyr	Ile	Ile	Thr	Gln	Val	Gly	Ser	Gly
	50					55					60				
Asp	Val	Asn	Asp	Arg	Val	Leu	Glu	Leu	Leu	Ile	Met	Ile	Asn	Ala	Ser
65					70					75					80
Lys	Thr	Ala	Ser	Ala	Arg	Arg	Ile	Thr	Ala	Val	Ile	Pro	Asn	Phe	Pro
				85					90					95	
Tyr	Ala	Arg	Gln	Asp	Arg	Lys	Asp	Lys	Ser	Arg	Ala	Pro	Ile	Thr	Ala
			100					105						110	
Lys	Leu	Met	Ala	Asp	Met	Leu	Thr	Thr	Ala	Gly	Cys	Asp	His	Val	Ile
		115					120					125			
Thr	Met	Asp	Leu	His	Ala	Ser	Gln	Ile	Gln	Gly	Phe	Phe	Asp	Val	Pro
	130					135					140				
Val	Asp	Asn	Leu	Tyr	Ala	Glu	Pro	Ser	Val	Val	Lys	Tyr	Ile	Lys	Glu
145					150					155					160
His	Ile	Pro	His	Asp	Asp	Ala	Ile	Ile	Ile	Ser	Pro	Asp	Ala	Gly	Gly
				165					170					175	
Ala	Lys	Arg	Ala	Ser	Leu	Leu	Ser	Asp	Arg	Leu	Asn	Leu	Asn	Phe	Ala
			180					185						190	
Leu	Ile	His	Lys	Glu	Arg	Ala	Lys	Ala	Asn	Glu	Val	Ser	Arg	Met	Val
		195					200					205			
Leu	Val	Gly	Asp	Val	Thr	Asp	Lys	Val	Cys	Ile	Ile	Val	Asp	Asp	Met
	210					215						220			
Ala	Asp	Thr	Cys	Gly	Thr	Leu	Ala	Lys	Ala	Ala	Glu	Val	Leu	Leu	Glu
225					230					235					240
His	Asn	Ala	Arg	Ser	Val	Ile	Ala	Ile	Val	Thr	His	Gly	Ile	Leu	Ser
				245					250					255	
Gly	Lys	Ala	Ile	Glu	Asn	Ile	Asn	Asn	Ser	Lys	Leu	Asp	Arg	Val	Val
		260						265					270		
Cys	Thr	Asn	Thr	Val	Pro	Phe	Glu	Glu	Lys	Met	Lys	Leu	Cys	Pro	Lys
		275					280					285			
Leu	Asp	Val	Ile	Asp	Ile	Ser	Ala	Val	Leu	Ala	Glu	Ser	Ile	Arg	Arg
	290					295					300				

Leu His Asn Gly Glu Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu  
305 310 315 320

<210> 14  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 14  
gatgctagag accgcggggt gcaac 25

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 15  
tgtccgccat gtcgtctaca ataata 26

<210> 16  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 16  
atatcttgat gaagacgttc accgt 25

<210> 17  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 17  
gataatgacg gcttggccgg gaaga 25

<210> 18  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 18

ggcatcaacc tcgaggaggc gaacc 25

<210> 19  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 19  
cagaccggcc tcgaccagca tcgcc 25

<210> 20  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 20  
tggaccgggc ggtgttcgag ttggg 25

<210> 21  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 21  
aggctggatc ctggctgcct cgcgc 25